listing references AI through AK and AM through BA together with a copy of references AI-BA; (10) a Supplemental Information Disclosure Statement with modified PTO Form 1449 listing references BB-BN together with a copy of references BB-BN; (11) a Petition for Extension of Time Under 37 C.F.R. § 1.13(b) for three months from September 1, 2001 to and including Monday, December 3, 2001, (December 1, 2001 being a Saturday) together with authorization for the necessary fee; and (12) a fee transmittal for authorization for any fees for amendments herein.

IN THE SPECIFICATION:

Please amend the specification to read as follows:

At page 10, delete the paragraphs describing Figures 5 and 6 beginning with "Figures 5..." and replace with the following:

Figure 5 A-E. Full length nucleotide sequence and corresponding deduced amino acid sequence of the PMPE polypeptide of *Chlamydia trachomatis* L2.

Figure 6 A-E. Full length nucleotide sequence and corresponding deduced amino acid sequence of the PMPI polypeptide of *Chlamydia trachomatis* L2.

At page 12, delete the paragraph beginning at line 23 which reads "As used herein a 'substantially homologous'..." and replace with the following:

As used herein a "substantially homologous" sequence is at least 70%, preferably greater than 80%, more preferably greater than 90% identical to a reference amino acid or nucleotide sequence of identical size or when compared to a reference sequence when the alignment or comparison is conducted by a computer homology program or search algorithm known in the art. By way of example and not limitation, useful computer homology programs include the following: Basic Local Alignment Search Tool (BLAST)

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(Altschul et al., 1990, J. of Molec. Biol., 215:403-410, "The BLAST Algorithm"; Altschul et al., 1997, Nuc. Acids Res. 25:3389-3402) a heuristic search algorithm tailored to searching for sequence similarity which ascribes significance using the statistical methods of Karlin and Altschul 1990, Proc. Nat'l Acad. Sci. USA, 87:2264-68; 1993, Proc. Nat'l Acad. Sci. USA 90:5873-77. Five specific BLAST programs perform the following tasks:

At page 13, delete the paragraph beginning at line 11 which reads "Smith-Waterman..." and replace with the following:

Smith-Waterman (database: European Bioinformatics Institute (Smith-Waterman, 1981, J. of Molec. Biol., 147:195-197) is a mathematically rigorous algorithm for sequence alignments.

At page 13, delete the paragraph beginning at line 14, which reads "FASTA (..." and replace with the following:

FASTA (see Pearson et al., 1988, Proc. Nat'l Acad. Sci. USA, 85:2444-2448) is a heuristic approximation to the Smith-Waterman algorithm. For a general discussion of the procedure and benefits of the BLAST, Smith-Waterman and FASTA algorithms see Nicholas et al., 1998, "A Tutorial on Searching Sequence Databases and Sequence Scoring Methods" and references cited therein.

At page 13, at line 33, delete the paragraph (through page 14, line 30) beginning with "The determination of percent ..." and replace with the following:

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm, a preferred, non-limiting example of a

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mathematical algorithm utilized for the comparison of two sequences is the algorithm of

Karlin and Altschul, 1990, <u>Proc. Nat'l Acad. Sci. USA</u>, 87:2264-68; as modified by 1993,

<u>Proc. Nat'l Acad. Sci. USA</u> 90:5873-77. Such algorithm is incorporated into the NBLAST

and XBLAST programs of Altschul, 1990, <u>J. of Molec. Biol.</u>, 215:403-410. BLAST

nucleotide searches can be performed with the NBLAST program, score = 100, wordlength =

12 to obtain nucleotide sequences homologous to a nucleic acid molecule of the invention.

BLAST protein searches can be performed with the XBLAST program, score = 50,

wordlength = 3 to obtain amino acid sequences homologous to a protein molecule of the

invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be

utilized as described in Altschul, 1997, <u>Nuc. Acids Res.</u> 25:3389-3402. Alternatively, PSI-

BLAST can be used to perform an iterated search which detects distant relationships between

molecules (*Id.*). When utilizing BLAST, Gapped BLAST, and PSI-BLAST programs, the

default parameters of the respective programs can be used. Another preferred, non-limiting

example of a mathematical algorithm utilized for the comparison of sequences is the

algorithm of Myers and Miller, CABIOS (1989). Such an algorithm is incorporated into the

ALIGN program (version 2.0) which is part of the CGC sequence alignment software

package. When using the ALIGN program for comparing amino acid sequences, a PAM120

weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

Additional algorithms for sequence analysis are known in the art and include ADVANCE and

ADAM as described in Torellis and Robotti (1994) <u>Comput. Appl. Biosc.</u>, 10:3-5; and

FASTA described in Pearson and Lipman, 1988, <u>Proc. Nat'l Acad. Sci. USA</u>, 85:2444-2448.

Within FASTA, ktup is a control option that sets the sensitivity and speed of the search. If

ktup = 2, similar regions in the two sequences being compared are found by looking at pairs

of aligned residues; if ktup = 1, single aligned amino acids are examined. Ktup can be set to